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Run on: September 20, 2002, 11:59:46 : Search time 14.07 seconds

(without alignments) 3.983 Million cell updates/sec

Title: us-08-971-172a-7

Scoring table: IDENTITY.NUC

Sequence: 1 ATGAAATGGAACATGTTC... TAGAGGAACGTAAAGCTCA 4956

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 5654 residues

number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : turner172.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Result No.	Query	Match Length	DB ID	Description
1	1997			Entered [sdavid 2]
c 1	4855.6	98.0	5654 1 ROBO_1997	Entered [sdavid 2]
c 2	22.4	0.5	5654 1 ROBO_1997	Entered [sdavid 2]

ALIGMENTS

Query Match 98.0% ; Score 4855.6; DB 1; Length 5654;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4855; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAATGGAACATGTTC... 60

Db 510 ATGAAATGGAACATGTTC... 569

QY 61 CACCTGTTCTGGCCGACTT... 120

Db 630 GGGACGCCATGCCAACCT... 689

Db 570 CACCTGTTCTGGCCGACTT... 629

QY 121 GGGACGCCATGCCAACCT... 180

Db 1710 TCATCGCCGATTTCAGTC... 1769

QY 181 CTGCTAGAAGAGATTCAC... 240

Db 690 CTCGCTAGAAGAGATTCAC... 749

QY 241 AAAGGAGAACCTGCAACTT... 300

QY 301 TGGTACAAGGGGGAGAGT... 869

Db 810 TGGTACAAGGGGGAGAGT... 869

QY 361 TTGCTGCCGAGTGGACTT... 420

Db 870 TTGCTGCCGAGTGGACTT... 929

QY 421 GATGAGGAGCTAGTCG... 540

Db 990 GCATGCTGGAGTAGCCACT... 1049

QY 541 GTTGAGTAGAGACCTG... 600

Db 1050 GTTGAGTAGAGACCTG... 1109

QY 601 ACCATTCTAGGAACAA... 660

Db 1110 ACCATTCTAGGAACAA... 1169

QY 661 CGAGGAGGAAGCTCAT... 720

Db 1170 CGAGGAGGAAGCTCAT... 1229

QY 721 GTTGAGPACCATATG... 780

Db 1230 GTTGAGPACCATATG... 1289

QY 781 AGACCATCATTTG... 840

Db 1290 AGACCATCATTTG... 1349

QY 841 TTAAATGTGAGGCCG... 900

Db 1350 TTAAATGTGAGGCCG... 1409

QY 901 GAGCCTGCCAAATCC... 960

Db 1410 GAGCCATCATTTG... 1469

QY 961 ACAGCTGGTACATGG... 1020

Db 1470 ACAGCTGGTACATGG... 1529

QY 1021 GCATCTGCTACTCTA... 1080

Db 1530 GCATCTGCTACTCTA... 1589

QY 1081 GTTGTGCTTGGCGACG... 1140

Db 1590 GTTGTGCTTGGCGACG... 1649

QY 1141 GCTATTTCGAGGAGA... 1200

Db 1650 GCTATTTCGAGGAGA... 1709

QY 1201 TCATCGCCGATTTCAG... 1260

Db 1710 TCATCGCCGATTTCAG... 1769

QY 1261 TCTGAGTGGTATTA... 1320

Db 1770 TCTGAGTGGTATTA... 1829

QY 1321 GCATTTGGAGATTCAC... 1380

Db 1830 GCATTTGGAGATTCAC... 1889

Db	4050	AACGGGGCAGACCTGCTTCCTCCCTCCACGCACATCCTCCUTCCACACAGCAATCGAA	4109	Db	5130	GTTGACATCGGAACAATTCCAGGTGATCCAGAGAACGACAGCAAATGACGG	5189
Qy	3601	GAGTACACATTTCTGTAGATGAAGCTATGACCAAGAAUTGCCATGTCCTGCCACCA	3660	Qy	4681	AAAGGACCTGGAACACGGCAAACGGAGACCTTCACCCAGCAAGACATCATCTC	4740
Db	4110	GAGTACACATTTCTGTAGATGAAGCTATGACCAAGAAUTGCCATGTCCTGCCACCA	4169	Db	5190	AAAGGACCTGGAACACGGCAAACGGAGACCTTCACCCAGCAAGACATCATCTC	5249
Qy	3661	GCAAGGAGTATTGACACAGATGAAGTAGAGAGGAGATGACGAGGCCACT	3720	Qy	4741	CAAGAGGAGTATTGACACAGGCAAACGGAGACCTTCACCCAGCAAGACATCATCTC	4800
Db	4170	GCAAGGAGTATTGACACAGATGAAGTAGAGAGGAGATGACGAGGCCACT	4229	Db	5250	CAAGAGGAGTATTGACACAGGCAAACGGAGACCTTCACCCAGCAAGACATCATCTC	5309
Qy	3721	CCCCCTGTCGGGAGAGCTTTCAGCAGGAGACTCAGGCCATGTACAGATGTCAG	3780	Qy	4801	CCAGTCTCCAACTCATGTCATCAAGAGGATCAGAAGCAGACAGAAC	4856
Db	4230	CCCCCTGTCGGGAGAGCTTTCAGCAGGAGACTCAGGCCATGTACAGATGTCAG	4289	Db	5310	CCCAGTCTCAAGCTCAATGTCATCAAGAGGATCAGGAGCACAAAGAAC	5365
Qy	3781	GCCACTCTGACTCCTCCCAAGAGAAGACTCAGGCCATGTACAGATGTCAG	3840				
Db	4290	GCCACTCTGACTCCTCCCAAGAGAAGACTCAGGCCATGTACAGATGTCAG	4349				
Qy	3841	GAGACTGGCCACTTGACGACCCGACAGGGACAGGGACAGGAGGAGGAGGAG	3900				
Db	4350	GAGACTGGCCACTTGACGACCCGACAGGGACAGGAGGAGGAGGAGGAG	4409				
Qy	3901	CCACCAAGGGCCAATCTGCCCTGCCACATCACATTTGGCTACATTTGAG	3950				
Db	4410	CCACCAAGGGCCAATCTGCCCTGCCACATCACATTTGGCTACATTTGAG	4469				
Qy	3961	GATTTGGATACGGATGCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG	4020				
Db	4470	GATTTGGATACGGATGCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG	4529				
Qy	4021	ATGCCAAACCAGAGGCTTGTGTTACGGGGCTTGTGAGACACCTGCTCC	4080				
Db	4530	ATGCCAAACCAGAGGCTTGTGTTACGGGGCTTGTGAGACACCTGCTCC	4589				
Qy	4081	GACCTGGAGAGCTCTGTCACSGGTCAATGATCAACCGCTSGGCTCAGC	4140				
Db	4590	GACCTGGAGAGCTCTGTCACGGGGCTCATGATCAACGGCTGGGCTAGCAG	4649				
Qy	4141	GACCAACATTCCAGCGGAGCCTGCACTGTTACTCTTGTGGGCTTTCAGT	4200				
Db	4650	GACCAACATTCCAGCGGAGCCTGCACTGTTACTCTTGTGGGCTTTCAGT	4709				
Qy	4201	GCTGACTTTGCCAGGAGTCGCCAGCAGGGAGATGCTGCTGAAGTAGCAG	4260				
Db	4710	GCTGACTTTGCCAGGAGTCGCCAGCAGGGAGATGCTGCTGAAGTAGCAG	4769				
Qy	4261	CGCCAATGCAAGGATGCTGCTGGCGTGTGACATTTGATGCCCTCTAGGCC	4320				
Db	4770	CGCCAATGCAAGGATGCTGCTGGCGTGTGACATTTGATGCCCTCTAGGCC	4829				
Qy	4321	ACAGATCCGCTGTACAGACAGAACATGAGTGCCCGTATGAGAACACGAC	4380				
Db	4830	ACAGATCCGCTGTACAGACAGAACATGAGTGCCCGTATGAGAACACGAC	4889				
Qy	4381	GCCAAAGAACCTGAAACACCGCCAGGACATCGCGAGAGAACCTACAGATG	4440				
Db	4890	GCCAAAGAACCTGAAACACCGCCAGGACATCGCGAGAGAACCTACAGATG	4949				
Qy	4441	CCACCACTCCCTGCCCCACCTGCTATAAGTCACCTACTGCCATCCAGACAG	4500				
Db	4950	CCACCACTCCCTGCCCCACCTGCTATAAGTCACCTACTGCCATCCAGACAG	5009				
Qy	4501	CNCGGAAGTACGACCTGTAGTGGGCCAAAACCTCCCTCTATGGATGCAAGAACGAC	4560				
Db	5010	CNCGGAAGTACGACCTGTAGTGGGCCAAAACCTCCCTCTATGGATGCAAGAACGAC	5069				
Qy	4561	TCTTCAGACAGAAAGGAGAGCTAACAGGGAGAGCTGGATGGAAGACAG	4620				
Db	5070	TCTTCAGACAGAAAGGAGAGCTAACAGGGAGAGCTGGATGGAAGACAG	5129				
Qy	4621	GTGACATGCGACAAMTCGCAAGGAGAGACACAGAACAAATGACGG	4680				

Search completed: September 20, 2002, 12:00:25
Job time: 39 sec

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